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## RAW SEQUENCE LISTING

DATE: 12/04/2002

PATENT APPLICATION: US/09/865,321A

TIME: 10:32:51

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Output Set: N:\CRF4\12032002\I865321A.raw

3 <110> APPLICANT: Peach, Robert J.  
 4 Naemura, Joseph R  
 5 Linsley, Peter S.  
 6 Bajorath, Jorgen  
 8 <120> TITLE OF INVENTION: SOLUBLE CTLA4 MUTANT MOLECULES AND USES THEREOF  
 10 <130> FILE REFERENCE: D0028PNP/30436.57USU1  
 12 <140> CURRENT APPLICATION NUMBER: 09/865,321A  
 13 <141> CURRENT FILING DATE: 2001-05-23  
 15 <150> PRIOR APPLICATION NUMBER: 60/287,576  
 16 <151> PRIOR FILING DATE: 2000-05-26  
 18 <150> PRIOR APPLICATION NUMBER: 60/214,065  
 19 <151> PRIOR FILING DATE: 2000-06-26  
 21 <160> NUMBER OF SEQ ID NOS: 9  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
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 28 <213> ORGANISM: Artificial Sequence  
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 62 ggcacgcgcta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180  
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66 gagctcatgt acccaccgcc atactacgag ggcataaggca acggaacca gatttatgta 420
67 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
68 acatccccac cgtccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
69 ccaaaacca aggacacct catgatctcc cggaccctg aggtcacatg cgtggtggtg 600
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71 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
72 gtcctcaccg tcctgcacca ggactggctg aatggcaagg agtacaagtg caaggctctc 780
73 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
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97 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
98 35 40 45
100 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
101 50 55 60
103 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
104 65 70 75 80
106 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
107 85 90 95
109 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
110 100 105 110
112 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
113 115 120 125
115 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
116 130 135 140
118 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
119 145 150 155 160
121 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
122 165 170 175
124 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
125 180 185 190
127 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
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134 225                      230                      235                      240
136 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
137                      245                      250                      255
139 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
140                      260                      265                      270
142 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
143                      275                      280                      285
145 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
146      290                      295                      300
148 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
149 305                      310                      315                      320
151 Gly Gln Pro Glu Asn Tyr Lys Thr Thr Thr Pro Val Leu Asp Ser
152                      325                      330                      335
154 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
155                      340                      345                      350
157 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
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175 ggcacgccta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
176 acagtgcctt gccaggctga cagccagggt actgaagtct gtgcggcaac ctacatgatg 240
177 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
178 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
179 gagctcatgt acccaccgcc atactacgag ggcataggca acggaaccca gatttatgta 420
180 attgatccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
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184 cataatgcca agacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
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186 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
187 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
188 ctgacctgcc tggtaaagg cttctatccc agcgacatcg ccgtggagtg ggagagcaat 960
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211           35           40           45
213 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
214           50           55           60
216 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
217           65           70           75           80
219 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
220           85           90           95
222 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
223           100          105          110
225 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
226           115          120          125
228 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
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231 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
232          145          150          155          160
234 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
235           165          170          175
237 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
238           180          185          190
240 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
241           195          200          205
243 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
244           210          215          220
246 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
247          225          230          235          240
249 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
250           245          250          255
252 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
253           260          265          270
255 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
256           275          280          285
258 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
259           290          295          300
261 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
262          305          310          315          320
264 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
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267 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
268          340          345          350
270 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
271          355          360          365
273 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
274          370          375          380
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321 20 25 30
323 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
324 35 40 45
326 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
327 50 55 60
329 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met

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**VERIFICATION SUMMARY**

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